

File  
On Hand

**RAW SEQUENCE LISTING**  
**ERROR REPORT**

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

09/663,600

Source:

1646 RUSH

Date Processed by STIC:

5/31/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

**Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/663,600

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) \_\_\_\_ contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) \_\_\_\_ missing. If intentional, please use the following format for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) \_\_\_\_ missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 10 ☐ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of "Artificial" (NEW RULES) Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.  
Valid response is Artificial Sequence.
- 12 ☐ Use of <220>Feature (NEW RULES) Sequence(s) \_\_\_\_ are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/663,600

DATE: 05/31/2001

TIME: 12:12:09

Input Set : D:\SEQLIST\Seqlist.txt

Output Set: C:\CRF3\05312001\I663600.raw

Does Not Comply  
Corrected Diskette Needed

4 <110> APPLICANT: Dumas Milne Edwards, Jean-Baptiste  
 5 Duclert, Aymeric  
 6 Bougueleret, Lydie  
 8 <120> TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS  
 10 <130> FILE REFERENCE: 31.US3.CIP  
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/663,600  
 C--> 13 <141> CURRENT FILING DATE: 2000-09-15  
 15 <150> PRIOR APPLICATION NUMBER: 60/066,677  
 16 <151> PRIOR FILING DATE: 1997-11-13  
 18 <150> PRIOR APPLICATION NUMBER: 60/069,957  
 19 <151> PRIOR FILING DATE: 1997-12-17  
 21 <150> PRIOR APPLICATION NUMBER: 60/074,121  
 22 <151> PRIOR FILING DATE: 1998-02-09  
 24 <150> PRIOR APPLICATION NUMBER: 60/081,563  
 25 <151> PRIOR FILING DATE: 1998-04-13  
 27 <150> PRIOR APPLICATION NUMBER: 60/096,116  
 28 <151> PRIOR FILING DATE: 1998-08-10  
 30 <150> PRIOR APPLICATION NUMBER: 60/099,273  
 31 <151> PRIOR FILING DATE: 1998-09-04  
 33 <160> NUMBER OF SEQ ID NOS: 229  
 35 <170> SOFTWARE: Patent.pm

## ERRORED SEQUENCES

12186 <210> SEQ ID NO: 228  
 12187 <211> LENGTH: 560  
 12188 <212> TYPE: DNA  
 12189 <213> ORGANISM: Homo sapiens  
 W--> 12190 <220> FEATURE:  
 12191 <221> NAME/KEY: CDS  
 12192 <222> LOCATION: (11)..(439)  
 W--> 12193 <220> FEATURE:  
 12194 <221> NAME/KEY: polyA\_site  
 12195 <222> LOCATION: (547)..(560)  
 W--> 12196 <220> FEATURE:  
 12197 <221> NAME/KEY: polyA\_signal  
 12198 <222> LOCATION: (530)..(535)  
 E--> 12199 <400> SEQUENCE: (229) 228 ← change to 228  
 12200 cagaacaatc atg tct gac tcc ctg gtg gtg tgc gag gta gac cca gag 49  
 12201 Met Ser Asp Ser Leu Val Val Cys Glu Val Asp Pro Glu  
 12202 1 5 10  
 12203 cta aca gaa aag ctg agg aaa ttc cgc ttc cga aaa gag aca gac aat 97  
 12204 Leu Thr Glu Lys Leu Arg Lys Phe Arg Phe Arg Lys Glu Thr Asp Asn  
 12205 15 20 25  
 12206 gca gcc atc ata atg aag gtg gac aaa gac cgg cag atg gtg gtg ctg 145  
 12207 Ala Ala Ile Ile Met Lys Val Asp Lys Asp Arg Gln Met Val Val Leu

see next page for more errors

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

FYI

**RAW SEQUENCE LISTING**

PATENT APPLICATION: US/09/663,600

DATE: 05/31/2001

TIME: 19:04:05

Input Set : C:\Jumbos\663600.txt

Output Set: C:\CRF3\05312001\I663600.raw

4 <110> APPLICANT: Dumas Milne Edwards, Jean-Baptiste  
5 Duclert, Aymeric  
6 Bougueleret, Lydie  
8 <120> TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS  
10 <130> FILE REFERENCE: 31.US3.CIP  
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/663,600  
C--> 13 <141> CURRENT FILING DATE: 2000-09-15  
15 <150> PRIOR APPLICATION NUMBER: 60/066,677  
16 <151> PRIOR FILING DATE: 1997-11-13  
18 <150> PRIOR APPLICATION NUMBER: 60/069,957  
19 <151> PRIOR FILING DATE: 1997-12-17  
21 <150> PRIOR APPLICATION NUMBER: 60/074,121  
22 <151> PRIOR FILING DATE: 1998-02-09  
24 <150> PRIOR APPLICATION NUMBER: 60/081,563  
25 <151> PRIOR FILING DATE: 1998-04-13  
27 <150> PRIOR APPLICATION NUMBER: 60/096,116  
28 <151> PRIOR FILING DATE: 1998-08-10  
30 <150> PRIOR APPLICATION NUMBER: 60/099,273  
31 <151> PRIOR FILING DATE: 1998-09-04  
33 <160> NUMBER OF SEQ ID NOS: 229  
35 <170> SOFTWARE: Patent.pm  
37 <210> SEQ ID NO: 1  
38 <211> LENGTH: 47  
39 <212> TYPE: RNA  
40 <213> ORGANISM: Artificial Sequence  
OK W--> 41 <220> FEATURE:  
42 <223> OTHER INFORMATION: in vitro transcription product  
W--> 43 <220> FEATURE:  
44 <221> NAME/KEY: modified\_base  
45 <222> LOCATION: 1  
OK W--> 46 <223> OTHER INFORMATION: m7g  
W--> 47 <400> SEQUENCE: 1  
48 ggcauccuac ucccauccaa uccacccua acuccucca ucuccac 47  
50 <210> SEQ ID NO: 2  
51 <211> LENGTH: 46  
52 <212> TYPE: RNA  
OK W--> 53 <213> ORGANISM: Artificial Sequence  
W--> 54 <220> FEATURE:  
55 <223> OTHER INFORMATION: in vitro transcription product  
W--> 56 <400> SEQUENCE: 2  
57 gcauccuacu cccauccaa uccacccuaa cuccuccau cuccac 46  
59 <210> SEQ ID NO: 3  
60 <211> LENGTH: 25  
61 <212> TYPE: DNA  
62 <213> ORGANISM: Artificial Sequence  
W--> 63 <220> FEATURE:  
64 <223> OTHER INFORMATION: oligonucleotide



invalid - give source of genetic material  
(see circled portion of item 12  
on Error Summary Sheet)

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

5/31/01